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Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

- 1. (Original) A method for the detection of a polymorphism in OATP8 in a human which method comprises:
- (i) determining the sequence of the human at any one of the following positions:

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positions 743, 811, 2021 and 2380 of SEQ ID NO: 16;
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positions 233 and 256 of SEQ ID NO: 17; or

(ii) determining the sequence of the human, wherein the human is a Caucasian human, at any one of the following positions:

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positions 389, 410 and 389-392 of SEQ ID NO: 15; positions 378, 1877 and 2501-2505 of SEQ ID NO: 16; position 112 of SEQ ID NO: 17.
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2. (Original) A method according to claim 1 wherein the polymorphism is further defined as:

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polymorphism at position 389 is presence of A and/or T;
polymorphism at position 410 is presence of T and/or A;
polymorphism at position 389-392 is presence of ATAT and/or TAGA;
polymorphism at position 743 is presence of A and/or G;
polymorphism at position 811 is presence of G and/or C;
polymorphism at position 2021 is presence of G and/or A;
polymorphism at position 2380 is presence of A and/or T;
polymorphism at position 378 is presence of G and/or T;
polymorphism at position 1877 is presence of A and/or G;
polymorphism at position 2501-2505 is presence of AAAAA and/or AAAAAA;
polymorphism at position 233 is presence of Ile and/or Met;
polymorphism at position 256 is presence of Gly and/or Ala; and
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polymorphism at position 112 is presence of Ser and/or Ala.

3. (Previously presented) A method according to claim 1 wherein the method for detection of a nucleic acid polymorphism is selected from amplification refractory mutation system and restriction fragment length polymorphism.

- 4. (Canceled)
- 5. (Original) A polynucleotide comprising at least 20 contiguous bases of the human OATP8 gene and comprising an allelic variant selected from any of the following:

Region	variant	Position
Exon 6	G	743 (SEQ ID NO: 16)
Exon 7	С	811 (SEQ ID NO: 16)
Exon 14	Α	2021 (SEQ ID NO: 16)
3' UTR	T	2380 (SEQ ID NO: 16)

- 6. (Original) An allele specific primer capable of detecting an OATP8 gene polymorphism at one of the following positions: positions 389, 410 and 389-392 of SEQ ID NO: 15; positions 743, 811, 2021, 2380, 378, 1877 and 2501-2505 of SEQ ID NO: 16.
- 7. (Original) An allele specific oligonucleotide probe capable of detecting a OATP8 gene polymorphism at one of the following positions: positions 389, 410 and 289-392 of SEQ ID NO: 15; positions 743, 811, 2021, 2380, 378, 1877 and 2501-2505 of SEQ ID NO: 16.
- 8. (Previously presented) A diagnostic kit comprising the allele-specific primer of claim 6.
- 9. (Original) A method of treating a human in need of treatment with a drug transportable by OATP8 in which the method comprises detection of a polymorphism in OATP8 in a human, which method comprises:
- (i) determining the sequence of the human at one of the following positions: positions 743, 811, 2021, 2380 of SEQ ID NO: 16;

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positions 233 and 256 of SEO ID NO: 17; or

determining the sequence of the human, wherein the human is a Caucasian human, at one of the following positions:

positions 389,410 and 389-392 of SEQ ID NO: 15;

positions 378, 1877 and 2501-2505 of SEQ ID NO: 16;

position 112 of SEQ ID NO: 17; and

ii) administering an effective amount of the drug.

- 10. (Canceled)
- 11. (Original) An allelic variant of human OATP8 polypeptide comprising:

a methionine at position 233 of SEQ ID NO: 17;

an alanine at position 256 of SEQ ID NO: 17;

an alanine at position 112 of SEQ ID NO: 17;

or a fragment thereof comprising at least 10 amino acids provided that the fragment comprises the allelic variant at position 233, 256 or 112 of SEQ ID NO: 17.

12. (Original) An antibody specific for an allelic variant of human OATP8 polypeptide as described herein having:

a methionine at position 233 of SEQ ID NO: 17;

an alanine at position 256 of SEQ ID NO: 17;

an alanine at position 112 of SEQ ID NO: 17;

or a fragment thereof comprising at least 10 amino acids provided that the fragment comprises the allelic variant at position 233, 256 or 112 of SEQ ID NO: 17.

- 13. (Original) A diagnostic kit comprising an antibody of claim 12.
- 14. (Previously presented) A diagnostic kit comprising the allele specific oligonucleotide probe of claim 7.

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NO:16; and

15. (New) A method for determining the presence or absence of a single nucleotide polymorphism (SNP) in an OATP8 gene, the method comprising:

- (a) providing a nucleic acid sample from a human identified as being in need of treatment with a therapeutic agent transportable by OATP8, wherein the sample comprises a nucleotide at each of the following nucleotide positions: positions 389, 389-392, and 410 as defined by the positions in SEQ ID NO:15; and positions 378, 743, 811, 1877, 2021, 2380, and 2501-2505 as defined by the positions in SEO ID
- (b) testing the sample to determine the identity of the nucleotide at one or more of the nucleotide positions.
- 16. (New) The method of claim 15, comprising determining the identity of the nucleotide at position 811 of SEQ ID NO:16.
- 17. (New) A method for determining the presence or absence of a SNP in an OATP8 gene, the method comprising:
- (a) providing a nucleic acid sample from a human identified as in need of treatment with a therapeutic agent transportable by OATP8, wherein the sample comprises a nucleotide at each of the following nucleotide positions:

positions 389, 389-392, and 410 as defined by the positions in SEQ ID NO:15; and positions 378, 743, 811, 1877, 2021, 2380, and 2501-2505, as defined by the positions in SEQ ID NO:16; and

- (b) testing the sample to determine the identities of all 17 nucleotides.
- 18. (New) A method for determining the presence or absence of a SNP in an OATP8 gene, the method comprising:
- (a) providing a nucleic acid sample from a human identified as in need of a drug transportable by OATP8, wherein the sample comprises a nucleotide at position 811 of the OATP8 gene as defined by the position in SEQ ID NO:16 and a nucleotide at at least one additional position selected from the group consisting of:

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positions 389, 410, and 389-392 as defined by the positions in SEQ ID NO:15; and positions 378, 1877, 2501-2505, 743, 2021, and 2380 as defined by the positions in SEQ ID NO:16; and

- (b) testing the sample to determine the identity of the nucleotide at one or more of the nucleotide positions.
- 19. (New) A method for determining the presence or absence of a single nucleotide polymorphism (SNP) in an OATP8 gene, the method comprising:
- (a) providing a nucleic acid sample from a human identified as in need of treatment with a therapeutic agent transportable by OATP8, wherein the sample comprises a nucleotide at a position corresponding to position 811 of SEQ ID NO:16; and
 - (b) testing the sample to determine the identity of the nucleotide.
- 20. (New) The method of claim 19, wherein the therapeutic agent is a statin.
- 21. (New) The method of claim 19, wherein step (b) comprises performing a technique selected from the group consisting of an ARMSTM, ALEXTM assay, COPS, TaqmanTM, Molecular Beacons, RFLP, restriction-site based PCR, and FRET.
- 22. (New) The method of claim 19, further comprising:
 - (c) determining that the nucleotide at position 811 is not a G.
- 23. (New) The method of claim 19, further comprising:
 - (c) determining that the nucleotide at position 811 is a C.
- 24. (New) The method of claim 19, wherein the nucleotide is in a codon that does not encode a glycine.
- 25. (New) The method of claim 19, wherein the nucleotide is in a codon that encodes an alanine.

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26. (New) The method of claim 19, further comprising:

(c) administering an effective amount of the therapeutic agent to the human.

- 27. (New) A method to assess the pharmacogenetics of a drug, the method comprising:
- (a) providing a nucleic acid sample from a human, wherein the sample comprises a nucleotide at a position corresponding to position 811 of SEQ ID NO:16;
 - (b) determining the identity of the nucleotide; and
- (c) correlating (i) the identity of the nucleotide to (ii) the human's response following administration of the drug, thereby assessing the pharmacogenetics of the drug.
- 28. (New) A method of treatment comprising:
- (a) identifying a patient in need of treatment with a therapeutic agent transportable by OATP8;
- (b) determining the identity of the nucleotide at the position corresponding to position 811 of SEQ ID NO:16 in a nucleic acid sample of the patient; and
- (c) administering to the patient an effective amount of a therapeutic agent transportable by OATP8, wherein the therapeutic agent is selected according to whether the nucleotide at the position corresponding to position 811 of SEQ ID NO:1 is a G or is not a G.
- 29. (New) The method of claim 28, wherein step (b) comprises:
- (i) providing a nucleic acid sample from the patient, wherein the sample comprises a nucleotide at a position corresponding to position 811 of SEQ ID NO:16; and
- (ii) determining the identity of the nucleotide by use of a method selected from the group consisting of an ARMSTM or ALEXTM assay, COPS, TaqmanTM, Molecular Beacons, RFLP, restriction site based PCR or FRET.
- 30. (New) The method of claim 28, wherein the nucleotide is not a G.
- 31. (New) The method of claim 28 wherein the nucleotide is a C.